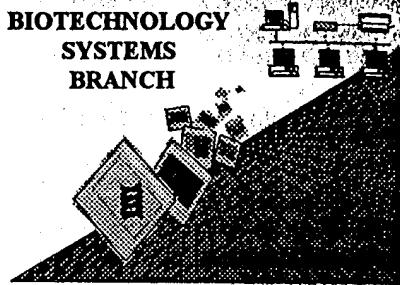


RAW SEQUENCE LISTING

ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 08/956,518

Art Unit / Team No. : 1645

Date Processed by STIC: 1/21/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

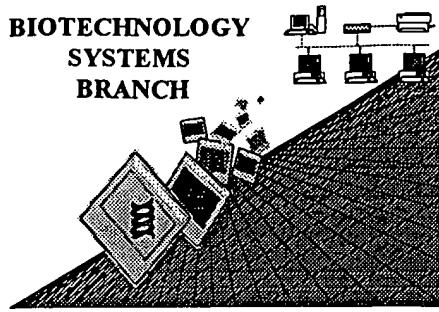
IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

BEST AVAILABLE COPY

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces. All text must be visible on page.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) ____ contain n's or Xaa's which represent more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) features section that some may be missing.	
7 <input type="checkbox"/> Wrong Designation	Sequence(s) ____ contain amino acid or nucleic acid designators which are not standard representations as per the Sequence Rules (Please refer to paragraph 1.822)	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Use of N's or Xaa's (NEW RULES)	Use of N's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present.	
11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)	Sequence(s) ____ are missing this mandatory field or its response.	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Sequence Rules)	
13 <input type="checkbox"/> Wrong Format	File submitted was in the alphabetical heading format of the Old Sequence Rules. This is invalid since the "Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures" Federal Register Notice, Vol. 63, No. 104, June 1, 1998, p. 29620 applies to applications filed on or after July 1, 1998.	



Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CRF 1.821 through 1.825).

Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested from the following locations:

- 1) Dial-up access through the Internet. Location is <ftp://ftp.uspto.gov>
The software is in current directory: pub/checker/
Download all the files. Cost: Free-of-charge
- 3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441
WASHINGTON DC 20231

COST FOR DISKETTE IS \$ 25.00

METHOD OF PAYMENT:

Check payable to Commissioner of Patents and Trademarks
VISA/ Mastercard/ Charge- Charges can be faxed to 703-306-2737
PTO Deposit Account

For Further Information, Contact: Arti Shah at 703-308-4212

R Hayes

1645

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/956,518

DATE: 01/21/99
TIME: 15:21:10

INPUT SET: S30866.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

1 SEQUENCE LISTING
2
3 (1) General Information:
4
5 (i) APPLICANT: Leonard, Sherry
6 Freedman, Robert
7
8 (ii) TITLE OF INVENTION: ALPHA-7 NICOTINIC RECEPTOR
9
10 (iii) NUMBER OF SEQUENCES: 121
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: MEDLEN & CARROLL, LLP
14 (B) STREET: 220 Montgomery Street, Suite 2200
15 (C) CITY: San Francisco
16 (D) STATE: CA
17 (E) COUNTRY: USA
18 (F) ZIP: 94104
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: US 08/956,518
28 (B) FILING DATE: 23-OCT-1997
29 (C) CLASSIFICATION:
30
31 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: MacKnight, Kamrin T.
33 (B) REGISTRATION NUMBER: 38,230
34 (C) REFERENCE/DOCKET NUMBER: UTC-03042
35
36 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: 415-705-8410
38 (B) TELEFAX: 415-397-8338
39
40

ERRORRED SEQUENCES FOLLOW:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/956,518

INPUT SET: S30866.raw

185 (2) INFORMATION FOR SEQ ID NO:9:

186

187

(i) SEQUENCE CHARACTERISTICS:

188

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

192

193

194

195

196

197

198

199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

200

201

AGATGCCCAA GTGGACCAGA GTCATCCTTC TGAACCTGGTG CGCGTGGTTC

-->

202

CTGCGAATGA 60

203

204

AGAGGCCCGG GGAGGACAAG GTGCGCCCGG CCTGCCAGCA CAAGCAGCGG

-->

205

CGCTGCAGCC 120

206

207

TGGCCAGTGT GGAGATGAGC GCCGTGGGCC CGCCGCCCGC CAGCAACGGG

-->

208

AACCTGCTGT 180

209

210

ACATCGGCTT CCGCGGCCCTG GACGGCGTGC ACTGTGTCCC GACCCCCGAC

-->

211

TCTGGGGTAG 240

212

213

TGTGTGGCCG CATGGCCTGC TCCCCCACGC ACGATGAGCA CCTCCTGCAC

-->

214

GGCGGGCAAC 300

215

216 CCCCCGAGGG GGACCCGGAC TTGGCCAAGA TCCTGGA

337

217

236

(2) INFORMATION FOR SEQ ID NO:11:

237

238

(i) SEQUENCE CHARACTERISTICS:

239

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

240

241

242

243

244

245

(ii) MOLECULE TYPE: other nucleic acid

246

- (A) DESCRIPTION: /desc = "DNA"

247

248

249

250

251

252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

253

CACACACACA TCACACACAC ACACACACAC ACACATACAC ACACACACCA CACA

54

254

(see item 1 on
Env summary sheet)

format env

60

120

same env

INPUT SET: S30866.raw

921 (2) INFORMATION FOR SEQ ID NO:49:
 922
 923 (i) SEQUENCE CHARACTERISTICS:
 --> 924 (A) LENGTH: 48 base pairs
 925 (B) TYPE: nucleic acid
 926 (C) STRANDEDNESS: single
 927 (D) TOPOLOGY: linear
 928
 929 (ii) MOLECULE TYPE: other nucleic acid
 930 (A) DESCRIPTION: /desc = "DNA"
 931
 932
 933
 934
 935 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
 936
 937 CAUCAUCAUC AUCCAGCGTA CATCGATGTA GCAGGAACTC TTGAATAT
 938 48
 939

940 (2) INFORMATION FOR SEQ ID NO:50:
 941
 942 (i) SEQUENCE CHARACTERISTICS:
 --> 943 (A) LENGTH: 41 base pairs
 944 (B) TYPE: nucleic acid
 945 (C) STRANDEDNESS: single
 946 (D) TOPOLOGY: linear
 947
 948 (ii) MOLECULE TYPE: other nucleic acid
 949 (A) DESCRIPTION: /desc = "DNA"
 950
 951
 952 (ix) FEATURE:
 953 (A) NAME/KEY: -
 954 (B) LOCATION: 32..33
 955 (D) OTHER INFORMATION: /note= "The residue at this
 956 position is Inosine."
 957
 958 (ix) FEATURE:
 959 (A) NAME/KEY: -
 960 (B) LOCATION: 36..37
 961 (D) OTHER INFORMATION: /note= "The residue at this
 962 position is Inosine."
 963
 964 (ix) FEATURE:
 965 (A) NAME/KEY: -
 966 (B) LOCATION: 41..42
 967 (D) OTHER INFORMATION: /note= "The residue at this
 968 position is Inosine."
 969
 970
 971 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

①? There are only 41 nucleic acids
in the sequence

same error

If you want
location 32 to be
Inosine, use "N."
Same with
location 33.

same error

Inosine can only be represented
by "N."

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/956,518

INPUT SET: S30866.raw

972
973 CUACUACUAC UAGGCCACGC GTCGACTAGT AC~~G~~~~G~~~~G~~GGG G
974 41
975

41

1570 (2) INFORMATION FOR SEQ ID NO:84:

1571

1572 (i) SEQUENCE CHARACTERISTICS:

--> 1573 (A) LENGTH: 55 base pairs
1574 (B) TYPE: nucleic acid
1575 (C) STRANDEDNESS: single
1576 (D) TOPOLOGY: linear

1577

1578 (ii) MOLECULE TYPE: other nucleic acid
1579 (A) DESCRIPTION: /desc = "DNA"

1580

1581

1582

1583

1584 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

1585

1586 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNCT
--> 1587 GCACG 55

1588

*Same
even*

1751 (2) INFORMATION FOR SEQ ID NO:94:

1752

1753 (i) SEQUENCE CHARACTERISTICS:

--> 1754 (A) LENGTH: 457 base pairs
1755 (B) TYPE: nucleic acid
1756 (C) STRANDEDNESS: single
1757 (D) TOPOLOGY: linear

1758

1759 (ii) MOLECULE TYPE: other nucleic acid
1760 (A) DESCRIPTION: /desc = "DNA"

1761

1762

1763

1764

1765 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

1766

1767 AGAACGCAAG GGAGAGGTAG AGCCTGGCCT TGGGCAGCCC CTGGCCTGGC
--> 1768 CAGAGCGCG 60

1769

1770 AGGCCGAGAG CCCGCTCGGT GGAGACTGGG GGTGGAGGTG CCCGGAGCGT
--> 1771 ACCCAGCGCC 120

1772

1773 GGGAGTACCT CCCGCTCACA CCTCGGGCTG CAGTTCCCTG GGTGGCCGCC
--> 1774 GAGACGCTGG 180

1775

1776 CCCGGGCTGG AGGGATGGCG GGGCGGGGAC GGGGGCGGGG GCGGGGCTCG
--> 1777 TCACGTGGAG 240

1778

Same

INPUT SET: S30866.raw

1779 AGGCGCGCGG GGGCGGGCGG GGCGGGGGCG CGCGCCCGGC TCCTTAAAGG
 --> 1780 CGCGCGAGCC 300
 1781
 1782 GAGCGGCGAG GTGCCTCTGT GGCGCGAGGC GCAGGCCCCGG GCGACAGCCG
 --> 1783 AGACGTGGAG 360 *Same*
 1784
 1785 CGCGCCGGCT CGCTGCAGCT CCGGGACTCA ACATGCGCTG CTCGCCGGGA
 --> 1786 GGCCTCTGGC 420
 1787
 1788 TGGCGCTGGC CGCGTCGCTC CTGCACGGTA AAGCCAC 457
 1789

1790 (2) INFORMATION FOR SEQ ID NO:95:
 1791
 1792 (i) SEQUENCE CHARACTERISTICS:
 --> 1793 (A) LENGTH: 308 base pairs
 1794 (B) TYPE: nucleic acid
 1795 (C) STRANDEDNESS: single
 1796 (D) TOPOLOGY: linear
 1797
 1798 (ii) MOLECULE TYPE: other nucleic acid
 1799 (A) DESCRIPTION: /desc = "DNA"
 1800
 1801
 1802
 1803
 1804 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:
 1805
 1806 CAGGCCGCCA CATAGCTCCC GCCAAGTCCT CGGTGCCCT TGCCATTTTC
 --> 1807 CAGCCCGCGTC 60 *Same*
 1808
 1809 CCACCGAGGGT CACGGCGCGG GGGAGAGGTG GAGCCGCCAG AGCTCGGCCG
 --> 1810 GGGGCCCGC 120
 1811
 1812 CTGGTGGCCG CGGCCATGAC AGCGGCTCGG GACTGGCTCC TTTCCGCC
 --> 1813 CCCTCCCGCC 180
 1814
 1815 GGAGGTGAGG GGAAGATGTC CATGTCAGGG TTCAAGGCCA AACCGAAGTT
 --> 1816 ACTGGCCCTC 240
 1817
 1818 TATCTTCCAG GAGAACCAAGG AGCCACAGCC GCGGCTCACG CCCCACCGCA
 --> 1819 ACATTAAGGT 300
 1820
 1821 GAGTCGCC 308
 1822

1823 (2) INFORMATION FOR SEQ ID NO:96:
 1824
 1825 (i) SEQUENCE CHARACTERISTICS:
 --> 1826 (A) LENGTH: 145 base pairs
 1827 (B) TYPE: nucleic acid
 1828 (C) STRANDEDNESS: single
 1829 (D) TOPOLOGY: linear

INPUT SET: S30866.raw

1830
1831 (ii) MOLECULE TYPE: other nucleic acid
1832 (A) DESCRIPTION: /desc = "DNA"
1833
1834
1835
1836
1837 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:
1838
1839 CTCATTTCA GATTACAAGTG GACACCTGAG TCAGCAGGAC CTGGAATCCC
--> 1840 AGATGAGAGA 60
1841
1842 GCTTATCTAC ACGACTCAGA TCTTGTGTC ACCCCCATTAA TTGACAATCC
--> 1843 AAAGGTGCAG 120
1844
1845 AAAGCACTCT GACAAGTGAG TTGTA 145
1846

None

1847 (2) INFORMATION FOR SEQ ID NO:97:
1848
1849 (i) SEQUENCE CHARACTERISTICS:
--> 1850 (A) LENGTH: 84 base pairs
1851 (B) TYPE: nucleic acid
1852 (C) STRANDEDNESS: single
1853 (D) TOPOLOGY: linear
1854
1855 (ii) MOLECULE TYPE: other nucleic acid
1856 (A) DESCRIPTION: /desc = "DNA"
1857
1858
1859
1860
1861 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:
1862
1863 TTAACCACAG ATAATGAAAC AACCAACCATC GGTTAAATTT GATGCAAAAA
--> 1864 TATTGCATCT 60
1865
1866 ACCAGCATTTCAGGTAGGA TCAT 84
1867

None

1868 (2) INFORMATION FOR SEQ ID NO:98:
1869
1870 (i) SEQUENCE CHARACTERISTICS:
--> 1871 (A) LENGTH: 67 base pairs
1872 (B) TYPE: nucleic acid
1873 (C) STRANDEDNESS: single
1874 (D) TOPOLOGY: linear
1875
1876 (ii) MOLECULE TYPE: other nucleic acid
1877 (A) DESCRIPTION: /desc = "DNA"
1878
1879
1880

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/956,518

INPUT SET: S30866.raw

1881
1882 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:
1883
1884 TTTATTCTAG TTCCAATTGC TAATCCAGCA TTTGTGGATA GCTGCAAACT
--> 1885 GCGATATGTA 60 *Name*
1886
1887 AGTAACA 67
1888

1889 (2) INFORMATION FOR SEQ ID NO:99:
1890
1891 (i) SEQUENCE CHARACTERISTICS:
--> 1892 (A) LENGTH: 100 base pairs
1893 (B) TYPE: nucleic acid
1894 (C) STRANDEDNESS: single
1895 (D) TOPOLOGY: linear
1896
1897 (ii) MOLECULE TYPE: other nucleic acid
1898 (A) DESCRIPTION: /desc = "DNA"
1899
1900
1901
1902
1903 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:
1904
1905 CTGTTTCTAG TGCTGATGAG CGCTTTGACG CCACATTCCA CACTAACGTG
--> 1906 TTGGTGAATT 60 *Name*
1907
1908 CTTCTGGGCA TTGCCAGTAC CTGCCTCCAG GTAAGCTGCA 100
1909

1928 (2) INFORMATION FOR SEQ ID NO:101:
1929
1930 (i) SEQUENCE CHARACTERISTICS:
--> 1931 (A) LENGTH: 392 base pairs
1932 (B) TYPE: nucleic acid
1933 (C) STRANDEDNESS: single
1934 (D) TOPOLOGY: linear
1935
1936 (ii) MOLECULE TYPE: other nucleic acid
1937 (A) DESCRIPTION: /desc = "DNA"
1938
1939
1940
1941
1942 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:
1943
1944 AGAACGCAAG GGAGAGGTAG AGCCTGGCCT TGGGCAGCCC CTGGCCTGGC
--> 1945 CAGAGGCGCG 60 *Name*
1946
1947 AGGCCGAGAG CCCGCTCGGT GGAGACTGGG GGTGGAGGTG CCCGGAGCGT
--> 1948 ACCCAGCGCC 120
1949

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/956,518

INPUT SET: S30866.raw

1950 GGGAGTACCT CCCGCTCACA CCTCGGGCTG CAGTTCCCTG GGTGGCCGCC
 --> 1951 **GAGACGCTGG** 180
 1952
 1953 CCCGGGCTGG AGGGATGGCG GGGCGGGGAC GGGGGCGGGG GCGGGGCTCG
 --> 1954 **TCACGTGGAG** 240
 1955
 1956 AGGCGCGCGG GGGCGGGCGG GGCGGGGGCG CGCGCCCGGC TCCTTAAAGG
 --> 1957 **CGCGCGAGCC** 300
 1958
 1959 GAGCGGCGAG GTGCCTCTGT GGCGCGAGGC GCAGGCCCCGG GCGACAGCCG
 --> 1960 **AGACGTGGAG** 360
 1961
 1962 CGCGCCGGCT CGCTGCAGCT CCGGGACTCA AC. 392
 1963

same

1964 (2) INFORMATION FOR SEQ ID NO:102:
 1965
 1966 (i) SEQUENCE CHARACTERISTICS:
 --> 1967 (A) LENGTH: 689 base pairs
 1968 (B) TYPE: nucleic acid
 1969 (C) STRANDEDNESS: single
 1970 (D) TOPOLOGY: linear
 1971
 1972 (ii) MOLECULE TYPE: other nucleic acid
 1973 (A) DESCRIPTION: /desc = "DNA"
 1974
 1975
 1976
 1977
 1978 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:
 1979
 1980 AGCCCTTTCC CAGGCGGTAG CGGGGGCAGT GGTGCTGTTG CCCTTTAAA
 --> 1981 **CTGCGGCTTG** 60
 1982
 1983 ACGGGAGCCG CGCCTCCTGT CGGTGGAGTC GGTTATAAAG GGAGCAGCCC
 --> 1984 **CGCAGGCCGC** 120
 1985
 1986 CACATAGCTC CCGCCAAGTC CTCGGTGCCC CTTGCCATTT TCCAGCCGCG
 --> 1987 **CTCCCCACGAG** 180
 1988
 1989 GGTACGGCG GCGGGGAGAG GTGGAGCCGC GAGAGCTCGG CCGGGGGCCC
 --> 1990 **CGCCTGGTGG** 240
 1991
 1992 CCGCGGCCAT GACAGCGGCT CGGGACTGGC TCCTTTCCG CGCCCTCCC
 --> 1993 **GCCGGAGGTG** 300
 1994
 1995 AGGGGAAGAT GTCCATGTCA GGGTTCAAGG CCAAACCGAA GTTACTGGCC
 --> 1996 **TCTATCTTCC** 360
 1997
 1998 AGGAGAACCA GGAGCCACAG CGCGGGCTCA CGCCCCACCG CAACATTAAG
 --> 1999 **ATTACAAGTG** 420
 2000
 2001 GACACCTGAG TCAGCAGGAC CTGGAATCCC AGATGAGAGA GCTTATCTAC

same

INPUT SET: S30866.raw

--> 2002 ACGACTCAGA 480
2003
2004 TCTTGTGTC ACCCCCCATTA TTGACAATCC AAAGGTGCAG AAAGCACTCT
--> 2005 GACAATTCCA 540
2006
2007 ATTGCTAATC CAGCATTGT GGATAGCTGC AAACTGCGAT ATTGCTGATG
--> 2008 AGCGCTTGA 600
2009
2010 CGCCACATTC CACACTAACG TGTTGGTGAA TTCTTCTGGG CATTGCCAGT
--> 2011 ACCTGCCTCC 660
2012
2013 AGGCATATTC AAGAGTTCCCT GCTACATCG 689
2014

2015 (2) INFORMATION FOR SEQ ID NO:103:
2016
2017 (i) SEQUENCE CHARACTERISTICS:
--> 2018 (A) LENGTH: 641 base pairs
2019 (B) TYPE: nucleic acid
2020 (C) STRANDEDNESS: single
2021 (D) TOPOLOGY: linear
2022
2023 (ii) MOLECULE TYPE: other nucleic acid
2024 (A) DESCRIPTION: /desc = "DNA"

Same

2025
2026
2027
2028
2029 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:
2030
2031 CAGGCCGCCA CATAGCTCCC GCCAAGTCCT CGGTGCCCT TGCCATTTC
--> 2032 CAGCCCGCGCT 60
2033
2034 CCCACGAGGG TCACGGCGGC GGGGAGAGGT GGAGCCGCGA GAGCTCGGCC
--> 2035 GGGGGCCCCG 120
2036
2037 CCTGGTGGCC CGGGCCATGA CAGCGGCTCG GGACTGGCTC CTTTCCGCG
--> 2038 CCCCTCCCCG 180
2039
2040 CGGAGGTGAG GGGAAAGATGT CCATGTCAGG GTTCAAGGCC AAACCGAAGT
--> 2041 TACTGGCCTC 240
2042
2043 TATCTTCCAG GAGAACCAAGG AGCCACAGCC GCGGCTCACG CCCCACCGCA
--> 2044 ACATTAAGAT 300
2045
2046 TACAAGTGGA CACCTGAGTC AGCAGGACCT GGAATCCCAG ATGAGAGAGC
--> 2047 TTATCTACAC 360
2048
2049 GACTCAGATC TTGTTGTCAC CCCCCATTATT GACAATCCAA AGGTGCAGAA
--> 2050 AGCACTCTGA 420
2051
2052 CAAATAATGA AACAAACCACC ATCGGTTAAA TTTGATGCAA AAATATTGCA
--> 2053 TCTACCAGCA 480

INPUT SET: S30866.raw

2054
 2055 TTTTCAGTTC CAATTGCTAA TCCAGCATT GTGGATAGCT GCAAACGTGCG
 --> 2056 ATATTGCTGA 540
 2057
 2058 TGAGCGCTTT GACGCCACAT TCCACACTAA CGTGTGGTG AATTCTTCTG
 --> 2059 GGCATTGCCA 600
 2060
 2061 GTACCTGCCT CCAGGCATAT TCAAGAGTTC CTGCTACATC G 641
 2062

2081 (2) INFORMATION FOR SEQ ID NO:105:
 2082
 2083 (i) SEQUENCE CHARACTERISTICS:
 --> 2084 (A) LENGTH: 140 base pairs
 2085 (B) TYPE: nucleic acid
 2086 (C) STRANDEDNESS: single
 2087 (D) TOPOLOGY: linear
 2088
 2089 (ii) MOLECULE TYPE: other nucleic acid
 2090 (A) DESCRIPTION: /desc = "DNA"
 2091
 2092
 2093
 2094
 2095 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:
 2096
 2097 TGTCCNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 --> 2098 NNNNNNNNNN 60
 2099
 2100 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 --> 2101 NNNNNNNNNN 120
 2102
 2103 NNNNNNNNNN NNNNGACGTG 140
 2104

Same

2123 (2) INFORMATION FOR SEQ ID NO:107:
 2124
 2125 (i) SEQUENCE CHARACTERISTICS:
 --> 2126 (A) LENGTH: 44 base pairs
 2127 (B) TYPE: nucleic acid
 2128 (C) STRANDEDNESS: single
 2129 (D) TOPOLOGY: linear
 2130
 2131 (ii) MOLECULE TYPE: other nucleic acid
 2132 (A) DESCRIPTION: /desc = "DNA"
 2133
 2134
 2135
 2136
 2137 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:
 2138
 2139 GATGAGNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNCA AATG
 2140 44

Same

INPUT SET: S30866.raw

2141

2160 (2) INFORMATION FOR SEQ ID NO:109:
2161
2162 (i) SEQUENCE CHARACTERISTICS:
--> 2163 (A) LENGTH: 110 base pairs
2164 (B) TYPE: nucleic acid
2165 (C) STRANDEDNESS: single
2166 (D) TOPOLOGY: linear
2167
2168 (ii) MOLECULE TYPE: other nucleic acid
2169 (A) DESCRIPTION: /desc = "DNA"
2170
2171
2172
2173
2174 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:
2175
2176 TCTTGGNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2177 NNNNNNNNNN 60
2178
2179 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNAACAG
2180 110
2181

Same

2200 (2) INFORMATION FOR SEQ ID NO:111:
2201
2202 (i) SEQUENCE CHARACTERISTICS:
--> 2203 (A) LENGTH: 80 base pairs
2204 (B) TYPE: nucleic acid
2205 (C) STRANDEDNESS: single
2206 (D) TOPOLOGY: linear
2207
2208 (ii) MOLECULE TYPE: other nucleic acid
2209 (A) DESCRIPTION: /desc = "DNA"
2210
2211
2212
2213
2214 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:
2215
2216 GCTGATNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2217 NNNNNNNNNN 60
2218
2219 NNNNNNNNNN NNNCCTCCAG
2220

Same

80

2239 (2) INFORMATION FOR SEQ ID NO:113:
2240
2241 (i) SEQUENCE CHARACTERISTICS:
--> 2242 (A) LENGTH: 168 base pairs
2243 (B) TYPE: nucleic acid
2244 (C) STRANDEDNESS: single

INPUT SET: S30866.raw

2245 (D) TOPOLOGY: linear
2246
2247 (ii) MOLECULE TYPE: other nucleic acid
2248 (A) DESCRIPTION: /desc = "DNA"
2249
2250
2251
2252
2253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:
2254
2255 GCATANNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2256 NNNNNNNNNN 60 *base*
2257
2258 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2259 NNNNNNNNNN 120
2260
2261 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NCTAGTGG
2262 168
2263

2282 (2) INFORMATION FOR SEQ ID NO:115:
2283
2284 (i) SEQUENCE CHARACTERISTICS:
--> 2285 (A) LENGTH: 195 base pairs
2286 (B) TYPE: nucleic acid
2287 (C) STRANDEDNESS: single
2288 (D) TOPOLOGY: linear
2289
2290 (ii) MOLECULE TYPE: other nucleic acid
2291 (A) DESCRIPTION: /desc = "DNA"
2292
2293
2294
2295

2296 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115: *base*
2297
2298 GAATCNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2299 NNNNNNNNNN 60
2300
2301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2302 NNNNNNNNNN 120
2303
2304 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2305 NNNNNNNNNN 180
2306
2307 NNNNNNNNTC CCTGG 195
2308

2327 (2) INFORMATION FOR SEQ ID NO:117:
2328
2329 (i) SEQUENCE CHARACTERISTICS:
--> 2330 (A) LENGTH: 87 base pairs
2331 (B) TYPE: nucleic acid

INPUT SET: S30866.raw

2332 (C) STRANDEDNESS: single
2333 (D) TOPOLOGY: linear
2334
2335 (ii) MOLECULE TYPE: other nucleic acid
2336 (A) DESCRIPTION: /desc = "DNA"
2337
2338
2339
2340
2341 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:
2342
2343 GGATANNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNN
--> 2344 NNNNNNNNNN 60
2345
2346 NNNNNNNNNN NNNNNNNNNN TTGATAG
2347

87

Name

2366 (2) INFORMATION FOR SEQ ID NO:119:
2367
2368 (i) SEQUENCE CHARACTERISTICS:
--> 2369 (A) LENGTH: 110 base pairs
2370 (B) TYPE: nucleic acid
2371 (C) STRANDEDNESS: single
2372 (D) TOPOLOGY: linear
2373
2374 (ii) MOLECULE TYPE: other nucleic acid
2375 (A) DESCRIPTION: /desc = "DNA"
2376
2377
2378
2379
2380 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:
2381
2382 CCCAGNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNN
--> 2383 NNNNNNNNNN 60
2384
2385 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNAAGTGG
2386 110
2387

Name

2406 (2) INFORMATION FOR SEQ ID NO:121:
2407
2408 (i) SEQUENCE CHARACTERISTICS:
--> 2409 (A) LENGTH: 519 base pairs
2410 (B) TYPE: nucleic acid
2411 (C) STRANDEDNESS: single
2412 (D) TOPOLOGY: linear
2413
2414 (ii) MOLECULE TYPE: other nucleic acid
2415 (A) DESCRIPTION: /desc = "DNA"
2416
2417
2418

INPUT SET: S30866.raw

2419
2420 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:
2421
2422 ACCAGANNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN
--> 2423 NNNNNNNNN 60
2424
2425 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN
--> 2426 NNNNNNNNN 120
2427
2428 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN
--> 2429 NNNNNNNNN 180
2430
2431 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN
--> 2432 NNNNNNNNN 240
2433
2434 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN
--> 2435 NNNNNNNNN 300
2436
2437 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN
--> 2438 NNNNNNNNN 360
2439
2440 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN
--> 2441 NNNNNNNNN 420
2442
2443 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN
--> 2444 NNNNNNNNN 480
2445
2446 NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNNNNN
2447 519
2448

Some

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/956,518

INPUT SET: S30866.raw

Line	Error	Original Text
188	Entered (337) and Calc. Seq. Length (87) differ	(A) LENGTH: 337 base pairs
202	# of Sequences for line conflicts w/ running total	CTGCGAATGA 60
205	# of Sequences for line conflicts w/ running total	CGCTGCAGCC 120
208	# of Sequences for line conflicts w/ running total	AACCTGCTGT 180
211	# of Sequences for line conflicts w/ running total	TCTGGGGTAG 240
214	# of Sequences for line conflicts w/ running total	GGCGGGCAAC 300
239	Entered (54) and Calc. Seq. Length (0) differ	(A) LENGTH: 54 base pairs
924	Entered (48) and Calc. Seq. Length (0) differ	(A) LENGTH: 48 base pairs
943	Entered (41) and Calc. Seq. Length (0) differ	(A) LENGTH: 41 base pairs
1573	Entered (55) and Calc. Seq. Length (5) differ	(A) LENGTH: 55 base pairs
1587	# of Sequences for line conflicts w/ running total	GCACG 55
1754	Entered (457) and Calc. Seq. Length (107) differ	(A) LENGTH: 457 base pairs
1768	# of Sequences for line conflicts w/ running total	CAGAGGCGCG 60
1771	# of Sequences for line conflicts w/ running total	ACCCAGCGCC 120
1774	# of Sequences for line conflicts w/ running total	GAGACGCTGG 180
1777	# of Sequences for line conflicts w/ running total	TCACGTGGAG 240
1780	# of Sequences for line conflicts w/ running total	CGCGCGAGCC 300
1783	# of Sequences for line conflicts w/ running total	AGACGTGGAG 360
1786	# of Sequences for line conflicts w/ running total	GGCGTCTGGC 420
1793	Entered (308) and Calc. Seq. Length (58) differ	(A) LENGTH: 308 base pairs
1807	# of Sequences for line conflicts w/ running total	CAGCCGCGTC 60
1810	# of Sequences for line conflicts w/ running total	GGGGCCCCGC 120
1813	# of Sequences for line conflicts w/ running total	CCCTCCCGCC 180
1816	# of Sequences for line conflicts w/ running total	ACTGGCCCTC 240
1819	# of Sequences for line conflicts w/ running total	ACATTAAGGT 300
1826	Entered (145) and Calc. Seq. Length (45) differ	(A) LENGTH: 145 base pairs
1840	# of Sequences for line conflicts w/ running total	AGATGAGAGA 60
1843	# of Sequences for line conflicts w/ running total	AAAGGTGCAG 120
1850	Entered (84) and Calc. Seq. Length (34) differ	(A) LENGTH: 84 base pairs
1864	# of Sequences for line conflicts w/ running total	TATTGCATCT 60
1871	Entered (67) and Calc. Seq. Length (17) differ	(A) LENGTH: 67 base pairs
1885	# of Sequences for line conflicts w/ running total	GCGATATGTA 60
1892	Entered (100) and Calc. Seq. Length (50) differ	(A) LENGTH: 100 base pairs
1906	# of Sequences for line conflicts w/ running total	TTGGTGAATT 60
1931	Entered (392) and Calc. Seq. Length (92) differ	(A) LENGTH: 392 base pairs
1945	# of Sequences for line conflicts w/ running total	CAGAGGCGCG 60
1948	# of Sequences for line conflicts w/ running total	ACCCAGCGCC 120
1951	# of Sequences for line conflicts w/ running total	GAGACGCTGG 180
1954	# of Sequences for line conflicts w/ running total	TCACGTGGAG 240
1957	# of Sequences for line conflicts w/ running total	CGCGCGAGCC 300
1960	# of Sequences for line conflicts w/ running total	AGACGTGGAG 360
1967	Entered (689) and Calc. Seq. Length (139) differ	(A) LENGTH: 689 base pairs
1981	# of Sequences for line conflicts w/ running total	CTGCGGCTTG 60
1984	# of Sequences for line conflicts w/ running total	CGCAGGCCGC 120
1987	# of Sequences for line conflicts w/ running total	CTCCCCACGAG 180
1990	# of Sequences for line conflicts w/ running total	CGCCTGGTGG 240
1993	# of Sequences for line conflicts w/ running total	GCCGGAGGTG 300
1996	# of Sequences for line conflicts w/ running total	TCTATCTTCC 360

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/956,518

INPUT SET: S30866.raw

Line	Error	Original Text
1999	# of Sequences for line conflicts w/ running total	ATTACAAGTG 420
2002	# of Sequences for line conflicts w/ running total	ACGACTCAGA 480
2005	# of Sequences for line conflicts w/ running total	GACAATTCCA 540
2008	# of Sequences for line conflicts w/ running total	AGCGCTTTGA 600
2011	# of Sequences for line conflicts w/ running total	ACCTGCCTCC 660
2018	Entered (641) and Calc. Seq. Length (141) differ	(A) LENGTH: 641 base pairs
2032	# of Sequences for line conflicts w/ running total	CAGCCGCGCT 60
2035	# of Sequences for line conflicts w/ running total	GGGGGGCCCCG 120
2038	# of Sequences for line conflicts w/ running total	CCCCTCCCGC 180
2041	# of Sequences for line conflicts w/ running total	TACTGGCCTC 240
2044	# of Sequences for line conflicts w/ running total	ACATTAAGAT 300
2047	# of Sequences for line conflicts w/ running total	TTATCTACAC 360
2050	# of Sequences for line conflicts w/ running total	AGCACTCTGA 420
2053	# of Sequences for line conflicts w/ running total	TCTACCAGCA 480
2056	# of Sequences for line conflicts w/ running total	ATATTGCTGA 540
2059	# of Sequences for line conflicts w/ running total	GGCATTGCCA 600
2084	Entered (140) and Calc. Seq. Length (40) differ	(A) LENGTH: 140 base pairs
2098	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2101	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 120
2126	Entered (44) and Calc. Seq. Length (0) differ	(A) LENGTH: 44 base pairs
2163	Entered (110) and Calc. Seq. Length (10) differ	(A) LENGTH: 110 base pairs
2177	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2203	Entered (80) and Calc. Seq. Length (30) differ	(A) LENGTH: 80 base pairs
2217	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2242	Entered (168) and Calc. Seq. Length (20) differ	(A) LENGTH: 168 base pairs
2256	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2259	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 120
2285	Entered (195) and Calc. Seq. Length (45) differ	(A) LENGTH: 195 base pairs
2299	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2302	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 120
2305	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 180
2330	Entered (87) and Calc. Seq. Length (37) differ	(A) LENGTH: 87 base pairs
2344	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2369	Entered (110) and Calc. Seq. Length (10) differ	(A) LENGTH: 110 base pairs
2383	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2409	Entered (519) and Calc. Seq. Length (80) differ	(A) LENGTH: 519 base pairs
2423	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2426	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 120
2429	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 180
2432	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 240
2435	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 300
2438	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 360
2441	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 420
2444	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 480